

Appl. No.: 10/796,307  
Atty. Docket: CL1509ORD

### AMENDMENTS TO THE CLAIMS

RECEIVED  
CENTRAL FAX CENTER

MAY 04 2007

This listing of claims will replace all prior versions, and listings of claims in the application.

#### Listing of claims

1. (Currently amended) A method for identifying ~~an individual~~ a human who has an altered risk for developing myocardial infarction, comprising detecting a single nucleotide polymorphism (SNP) as represented by ~~a the~~ nucleotide sequence ~~selected from the group consisting of SEQ ID NOs 33944, 21614, 36349, 25917, 21749, 29108, 27819, 10810, 11670, 28735~~ in said ~~individual's~~ human nucleic acids, wherein the presence of the SNP is correlated with an altered risk for myocardial infarction in said ~~individual~~ human.

2. (Original) The method of claim 1 in which the altered risk is an increased risk.

3. (Original) The method of claim 2 in which said individual has previously had a myocardial infarction.

4. (Original) The method of claim 1 in which the altered risk is a decreased risk.

5. (Canceled)

6. (Original) The method of claim 1 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

7.-20. (Canceled)

21. (Currently amended) A method of detecting a single nucleotide polymorphism (SNP) in a nucleic acid molecule, comprising contacting a test sample with a reagent which specifically

Appl. No.: 10/796,307  
Atty. Docket: CL1509QRD

hybridizes to a the SNP as represented by a the nucleotide sequence ~~selected from the group~~ consisting of SEQ ID NOs 33944, ~~21614, 36349, 25917, 21749, 29108, 27819, 10810, 11670, 28735~~ under stringent hybridization conditions, and detecting the formation of a hybridized duplex, thereby indicating the presence of said SNP.

22. (Original) The method of claim 21 in which detection is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

23.-24. (Canceled)